

BIOTECHNOLOGY

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	= 29/9/0, 20 XV
Source:	, 16.2 Kasit
Date Processed by STIC:	10/21/202 -

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER **VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual - ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- 3. Hand Carry directly to: U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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Revised 01/29/2002

Raw Sequence Listing Error Summary

- DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/7/0,2620
ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/1/0, 26 CO
ATTN: NEW RULES CASES	E: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
0Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
1Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
2PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
3Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/710,262D

DATE: 10/21/2002 TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw Output Set: N:\CRF4\10212002\1710262D.raw

```
Ron, Eliora
      3
              Orr, Elisha
              Paitan, Yossi
      5 <120> TITLE OF INVENTION: GENE CLUSTER
      6 <130> FILE REFERENCE: 2290.00101
CX-> 7 <140> CURRENT APPLICATION NUMBER: US/09/710,262D
      8 <141> CURRENT FILING DATE: 2000-11-10
      9 <160> NUMBER OF SEQ ID NOS: 20
     10 <170> SOFTWARE: PatentIn Ver. 2.1
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1 <110> APPLICANT: Rosenberg, Eugene

Corrected Diskette Needed

Markette Needed

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ERRORED SEQUENCES

	12	<210><211><211><212><213>	SEQ	ID	NO:	1					0	٨	1			Rul)		
	1.3	<211>	LEN	GTH:			> 6	RT	01	۸ L.	825	· /\	Ae	juer	u.	,,,,,,,,	~		A
	14	<212>	TYP	E:(A)	mino	acı	ارو			- -	•	/	ı	y			+		- () ()
01						ухос	occu	S Xa	nunu	S									19404
رع) ح		<400>				7 l n	7 ~~	T 011	mb~	7 200	7 l ~	m-m	C1.,	C1	T OU	T 011	Clu	λκα	(amos)
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	18 19		Ш.т.ж	Dwo	т о и	Tou	71a	C1	7 1 a	т1.			Clu	C1**	-			17 - 1	
			тут	PIO		_ьец 20- э	Ala	GT.	Αįα		35	vа́т	Gin	Gly -30		30	PIO	٧a٫ı	misaligned
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	22		iire		5 3S	Ser	GTA	ĠŤII	4.0	40	Ala	Gin	•		45	vaı	PIO	ser	amiro ava
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	25		١.		AGD	LOU	λ15		-	Pro	LAU	λla		Leu	Uic	LAU	Tur.	Sar	() = 0
	26		65	PHE	rsb	ьеи		70	GIY	FIU	пеп	75	ліч	пец	птэ	пец	80	Ser	(sel item 3
	27			Sar	Glu	шie			Val-	_T.011	-T-011-		- 	Phe	His	His	T.OU	Val	(Jul None)
	28		nry-				85	-1113	Val	Бец	90	пец	Cys	riic	1113	-9 5	1000	, var	on Ever
	29		T.e.u	Δen	Glv			ิงสา	Δla	Pro		T.eu	Asn	Ala	T.e.11		Glu	Ara	on our
	30		пси	nsp		100	001	, ,	niu	10		ДСи	ПОР		10-			9	1
	31		Tvr	Δla	7		GIII	Ala	LVS			Leu	Leu	Glu	Val	Pro	Tle	Val	Sunnay
	32		-1-	(1)	-		014		120		0-1			25					, ,
	33		Ala	<u>_</u>		Ara	Ala	Ala		Glu	Trp	Glu	Gln	Leu	Ala	Ile	Glv	Glv	(/ . 4)
	34			130	-1			135					10				1	1	Stell
	35				Gly	Arq	Arq	His	Leu	Asp	Tyr	Trp	Arq	His	Val	Leu	Ala	Thr	
	36		145		-	7	_	50		-	•	155				- 16			
	37		Pro	Val	Pro	Pro	Pro	Leu	Asn	Leu	Pro	Thr	Asp	Arg	Pro	Arg	Ser	Ala	
	38					1					170					75			
	39		Thr	Gly	Leµ.	. Asp	Ser	Glu	Gly	Ala	Thr	His	Ser	Gln	Arg	Val	Pro	Thr	
	40			-		180			-	185				19	-				
					\ -										_				

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

41 42	Glu		Ala 195	Leu	Arg	Leu	Arg 200		Phe	Ala	-	Ala 205	Gln	Gln	Val	Ser
43 44		Pro 210	Thr	Val	Leu		Gly 15	Leu	Tyr		Ala 220	Leu	Leu	His	Arg	His
45 46			Gln	Asp	~		Val	Val	_			Thr	Met	Gly 240	-	Pro
47		Ala	Glu		Ala		Ala		Gly		Phe	Val		Val		Ala
48	17 n 1	7 ~~	712		15	LOU	Gly		250 Hic	Sor	Dho	Clv	255		Lau	λνα
49 50	Val	Arg		60 60	GTĀ	Deu	GIY	265	1113	361	FIIC		270	Беи	Deu	nry
51	His			Asp	Ser	Val	Ile	Asp	Gly	Leu			Ala	His	Tyr	Pro
52			275	_	_		280					35		_	_ •	
53	Phe		Arg	Val	Val	_	_	Leu	Arg	Leu		Asn	GLY	Pro	GIu	Glu
54		290	~ 1	_,	~1		95	-1	-1	-,	300			6 3	.	m1
55		Pro	GLY	Phe			Met	Phe	Thr			Ser	Leu			Thr
56	305		_	_		L0		_	_	315		- 1	_		320	_
57	Ser	Ala	Pro		_	Pro	Glu	Pro		Ser	GTA	GTA			Glu	Leu
58	_				25				330			_		335		_
59	Glu	Pro		_	Cys	Val	His			GTA	Ala	_		Leu	GIU	Leu
60	_	_		340			•	34			_		350	_	_	_
61	Glu			Glu	GLy	Ala	Lys	_	Leu	Thr			Phe	Lys	Tyr	Asp
62			355				360					55		_		_
63			Leu	Tyr	Glu		Asp	Thr	Val			Met	Ala	Arg	GIn	Leu
64		370				375		_			380_	_				_
65		Arg	Ala	Ala	-		Val	Ala	_	-	Val	Glu	Ser			Ser
66	385					90		_		395					00	
67	Ala	Leu	Ser	_		Asp	Asp	Glu			Arg	Thr	Leu		Arg	Asp
68			_)5_				410	-	_	_		415	•	~ 1
69	Trp	Asn			Ala	Thr	Pro			G⊥u	Asp			Val	His	GIu
70				120			_	42		_	_		130			~
71	Leu	Phe		Arg	GIn	Ala	Arg		Thr	Pro	Asp		Met	Ala	vaı	ser
72	_		435	•	_	_		10	~ 1		_	445	m1	_	~	
73	_		GIY	His	Ser		Ser	Tyr	GIn			Asp	Thr	Arg	ser	Arg
74		150				45			51 .		160		n	a 1		.
75		TTE	Ата	Ата		Leu	Lys	ser			vaı	ьys	Pro		Ата	Leu
76	465	~ 3	- 1	_	470		•	a		75	.	17 - 1		480	36-4	T
77	Val	GIĀ	тте			Asp	Arg			GIU	ьеu	vaı			мет	Leu
78			_	485					190		.	- .	495		**- 1	***
79	GLY	Val	_		Ala	GIŸ	Ala		Tyr	val	Pro			Pro	vaı	HIS
80	D	a 1		500	T	3	m	505	T	~1	3	53		17 n 1	170 1	1707
81	Pro			Arg	Leu	Arg	Tyr		ьeu	GIU	Asp		GIY	vaı	val	val
82	** - 1		515	•	01	3 1 -	520		>	T	17-1	525		T1_	7.1.0	01
83			Ата	Arg	GIn		Ser	Arg	ASP			Ата	Ата	TTE	Ald	GIY
84		30	O+	T	37-1	535		T 0	C1		340	T~	77~	C1	λl ¬	πh∽
85		ser	Cys	гаг			Val	ьeu	GIU		val	пλг	нта			TIIT
86	545	7 l ~	Dro	7 J -	55		C0~	Dro	λ α ~	555	T 011	7 J ¬	Птт∽	56 v=1		ጥ፣ታው
87	ser	нта	PLO		-	T IIT.	Ser	PLO	570	сту	ьeu	HIG		_	TTE	тАт
88	Th∽	e~~	C1.,	56		C157	λνα	Dro		G1 vr	V=1	Mo+	575		Hie	Δrα
89	THE	Set	атў	ser.	TIIT	ату	Arg	PIO	пЛр	оту	val	Me C	Tie	FIU	UTD	лгу

Jame Le Mo

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

90	580 585 590	
91	Gly Val Val Asn Phe Leu Leu Cys Met Arg Arg Thr Leu Gly Le	eu Lys
92	595 600 605	-
93	Arg Thr Asp Ser Leu Leu Ala Val Thr Thr Tyr Cys Phe Asp II	le Ala
94	610 615 620	
95	Ala Leu Glu Leu Leu Pro Leu Cys Ala Gly Ala Gln Val I	le Ile
96	625 630 635 640	
97	Ala Ser Ala Glu Thr Val Arg Asp Ala Gln Ala Leu Lys Arg Al	la Leu
98	645 650 655	
99	Arg Thr His Arg Pro Thr Leu Met Gln Ala Thr Pro Ala Thr Tr	rp Thr
100	660 665 670	
101	Leu Leu Phe Gln Ser Gly Trp Glu Asn Ala Glu Arg Val Arg	Ile Leu
102	675 680 685	
103	Cys Gly Glu Ala Leu Pro Glu Ser Leu Lys Ala His Phe V	Val Arg
104	690 695 700	
105	Thr Ala Ser Asp Val Trp Asn Met Phe Gly Pro Thr Glu Thr	
106	705 710 715 720	
107	Trp Ser Thr Met Ala Lys Val Ser Ala Ser Arg Pro Val Thr	Ile Gly
108	725 730 735	
109	Lys Pro Ile Asp Asn Thr Gln Val Tyr Val Leu Asp Asp Arg N	Met Gin
110	740 745 750	.1- 01
111	Pro Val Pro Ile Gly Val Pro Gly Glu Leu Trp Ile Ala Gly 1	Ala Giy
112	755 760 765	Ara Dho
113	Val Ala Cys Gly Tyr Leu Asn Arg Pro Ala Leu Thr Ala Glu A	arg Phe
114	770 775 780 Val Ser Asn Pro Phe Thr Pro Gly Thr Thr Leu Tyr Arg Thr (clu Acn
115 116	785 790 795 800	
117	Leu Ala Arg Trp Arg Ala Asp Gly Glu Val Glu Tyr Leu Gly	_
118	805 810 815	iii y Deu
119	Asp His Gln Val Lys Val Arg Gly Phe Arg Ile Glu Met Gly (Glu Ile
120	820 825 830	
121	Glu Ala Gln Leu Ala Gly His Pro Ser Val Lys Asn Cys Ala V	Val Val
122	835 840 845	
123	Ala Lys Glu Leu Asn Gly Thr Ser Gln Leu Val Ala Tyr Cys (Gln Pro
124	850 855 860	
125	Ala Gly Thr Ser Phe Asp Glu Glu Ala Ile Arg Ala His Leu A	Arg Lys
126	865 870 875 880	
127	Phe Leu Pro Asp Tyr Met Val Pro Ala His Val Phe Ala Val A	Asp Ala
128	885 890 895	
129	Ile Pro Leu Ser Gly Asn Gly Lys Val Asp Arg Gly Gln Leu M	Met Ala
130	900 905 910	
131	Arg Pro Val Val Thr Arg Arg Lys Thr Ser Ala Val His Ala A	Arg Ser
132	915 920 925	
133	Pro Val Glu Ala Thr Leu Val Glu Leu Trp Lys Asn Val Leu (Gln Val
134	930 935 940	
135	Asn Glu Val Gly Val Glu Asp Arg Phe Phe Glu Val Gly Gly A	
136		60
137	Val Leu Ala Ala Val Leu Val Glu Glu Met Asn Arg Arg Phe	asp Thr
138	965 970 975	

same

Input Set : N:\Crf4\10182002\I710262D.raw Output Set: N:\CRF4\10212002\I710262D.raw

139	Arg Leu	Ala Va		Asp	Leu	Phe 98	_	Tyr	Val		Ile 90	Arg	Asp	Met	
140 141	Ala Arg			Glv	Δla			Gln	Δla			Glv	Δla	Thr	
142	-	995	0	OLY	100		niu	01	100	-		G = 1			
143	Glu Pro		g Glu	Asp			Ser	Glu	-		Tyr	Glu	Gly	Ser	
144	1010		,	10					1020	•	-		-		
145	Leu Ala	Val I	e Gly	Ile	Ser	Cys	Gln	Leu	Pro	Gly	Ala	Ala	Asp	Pro	
146	1025		1030				10	35				1040			
147	Trp Arg	Phe Ti	p Lys	Asn	Leu	Arg	Glu	Gly	Arg	Asp	Ser	Val	Val	Ala	
148			1045				10					1055			
149	Tyr Arg			Leu	Arg			Gly	Val			Glu	Val	Leu	
150		1060				106					070			_	
151	Arg Asp		g Tyr	Val			Arg	Ser			Glu	Asp	Lys	Glu	
152		1075			108			_	10				_		
153	Cys Phe	Asp Pi	o His			GLy	Leu	Thr			Asp	Ala	Ser	Phe	
154	1090				095	_	_		1100		_	_			
155	Met Asp	Pro G		_	Leu	Leu	Leu			Ala	Trp			Val	
156	1105		1		.	01		11.		5	a		120	Dl	
157	Glu Asp	Ala Al		Thr	Pro		_	Leu	GIY	Pro	_	_	vaı	Pne	
158	Mat mb-	. 1 - 0.	1125	a	Dh.a		1130	a1.	G1			135	Dha	Dwo	
159	Met Thr			ser	Pne	114		GIII	GIY			GIII	Pne	PIO	
160	715 705	1140		1751	Tou		_	71.	C1.,		150	Wa I	T 011	Tro	
161 162	Ala Asp	GIY GI 1155	n Pro	vaı	1160	-	THE	Ald		165	TAT	vaı	Leu	пр	
163	Val Leu		n Ala	C117			Dro	mh r			Cor	Ttr	Tuc	Lou	-
164	1170	ALA GI	.II AIa	117		ire	PIO	111		vai	ser	тут	пÃ2	Leu	
165	Gly Leu	Tyc Cl	v Dro			Dho	V = 1			Δen	Cve	Sor	Sar	Ser	
166	1185	пуз ол	.y F10		цец	FIIE		L195	1111	NSII	Cys		200	Ser	
167	Leu Ser	Δla T.e			Δla	Gln			T۱۵	Δla	Δla			Cvs	
168	neu bei	AIG DO	1205	141	niu		1210	ALU	110		1215	011	пор	CID	
169	Gln Thr	Ala Le	-	G1v	Ala			Va 1	Phe			Ala	Asn	Leu	
170	OIN INI	1220		O.L.y		1225	1111	V (4.1.	1 110	123			11011		
171	Gly Tyr			Arg			Asn	Phe	Ser			Glv	Ara	Val	
172		235		5	1240					L245		1	5		
173	Lys Ala		p Ala	Ala			Gly	Met	Ile	Ala	Gly	Glu	Gly	Val	
174	1250		•	12		-	-		260		-		-		
175	Ala Val	Leu Va	l Val			Ala	Ala	Ala	Ala	Val	Arg	Asp	Gly	Asp	
176	1265		12		_			275			_	1280			
177	Pro Ile	Tyr Cy	s Leu	Val	Arg	Lys	Val	Gly	Ile	Asn	Asn	Asp	Gly	Gln	
178		1	285				1290				1295	5			
179	Asp Lys	Val Gl	y Leu	Tyr	Ala	Pro	Ser	Ala	Thr	Gly	Gln	Ala	Glu	Val	
180		1300				130	5			133	LO				
181	Ile Arg	Arg Le	u Phe	Asp	Arg	Thr	Gly	Ile	Asp	${\tt Pro}$	Ala	Ser	Ile	Gly	
182	13	315			1320)			132	25					
183	Tyr Val	Glu Al	a His	Gly	Thr	Gly	Thr	Leu	Leu	Gly	Asp	Pro	Val	Glu	
184	1330			133					340						
185	Val Ser	Ala Le			Ala	Phe	_		Phe	Thr	Asp	Arg	Arg	Gly	
186	1345		13					L355				136			
187	Tyr Cys	Arg Le	u Gly	Ser	Val	Lys	Ser	Asn	Leu	Gly	His	Leu	Asp	Thr	

same

1) always space between last amino acid number and next amino acid

Input Set : N:\Crf4\10182002\1710262D.raw
Output Set: N:\CRF4\10212002\1710262D.raw

188	1365	5	1370	1375
189				Leu Ser Leu Arg Gln
190	1380	ia oij ioa	1385	1390
191		ro Thr Leu		Val Asn Pro Lys Leu
192	1395		400	1405
193				Arg Leu Ala Pro Trp
194	1410	141	_	420
195			· -	Ser Ala Phe Gly Leu
196		1430	1435	1440
197				Tyr Pro Arg Asp Ser
198	1445		1450	1455
199				Val Arg Ala Val Ala
200	1460		1465	1470
201				Asp Asn Leu Arg Ala
202	1475	148		1485
203				Glu Val Ala Leu Ala
204	1490	1495	150	
205				Ala Met Pro Glu Arg
206		510	1515	1520
207				Val Glu Gly Leu Arg
207	1525	la sei illi	1530	1535
209		hr Val Cly		Gly Thr Val Val Asp
210	1540			1550
210				Val Ala Glu Ala Trp
212	1555	1560		=
212				His Gly Asp Val Lys
213	1570	1575	1580	his diy Asp vai hys
214				Ala Lys Glu Arg Tyr
216		590	1595	1600
217				Ser Lys Thr His Pro
218	1605		1610	1615
219				Gln Pro Trp Ser Glu
220	1620		1625	1630
221				Leu Val Val Leu Cys
222	1635	1640	_	545
223				Ser Ala Leu Ala Ser
224	1650	1655	1660	ber ma ber
225				Thr Ser Ser Pro Ser
226	-	1670	1675	1680
227				Ser Ala Val Phe Glu
228	1685		1690	1695
229				Ala Pro Val Thr Leu
230	1700		1705	1710
231				Ala Leu Ser Gly Leu
232	1715	1720		725
233				Pro Leu Val Arg Gly
234	1730	1735	1740	311
235				Ser Ala Leu Val Asp
236	_	750	1755	1760
			55	

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

237 238	Val Leu	_	Ser Al	la Arg	Ala Gly 1770	_	l Thr	Asp Ser	Arg	Tyr
239 240	His Ala	Gly Gln 1780	Leu Se	er Arg	Cys Glu 1785	Trp Ar		Ala Arg '90	Val	Ala
241 242	Lys Gly		Ser Ar	rg Phe 180		Glu As	9 Gly 1805	Val Tyr	Val	Ile
243 244	Ser Gly 1810	Gly Thr	_			Leu Ph		Ala Glu	Ile	Gly
245 246	Lys Arg 1825	Ala Thr	Arg Al 1830	la Thr		Leu Va 35	l Ala	Arg Ala 1840	Ser	Ser
247 248	Ala Glu	Ala Val	-	ly Gly	Asn Gly 1850	•	y Val	Arg His 1855	Leu	Pro
249 250	Val Asp	Val Thr 1860	Gln Pr	co Asn				Val Ala 870	Thr	Val
251 252	Leu Arg		Gly Ar	rg Ile 1880	Asp Gly	Val Il		Ala Ala	Gly	Ile
253 254	Arg Arg 1890	Asp Asn	_	eu Leu 1895	Asn Lys	Pro Va 190		Glu Met	Gln	Ala
255 256	Val Leu 1905	Ala Pro	Lys Va 1910	al Val	_	Val As: 915	n Leu	Asp His		Thr
257 258	Arg Glu			sp Phe		Thr Ph	e Ser	Ser Leu 1935	Ala	Ala
259 260	Phe Gly			ln Ser					Phe	Met
261 262	Asp Gly		Glu Se	er Arg	Ala Ala				Gln	Arg
263 264	Gln Gly 1970							Glu Asn	Gly	Gly
265 266	Met Gln 1985	Leu Asp		rg Ser	Arg Glu		ı Met		Thr	Gly
267 268	Met Ala				Ala Gly 201	Leu Gl	y Ala			Ala
269 270	Leu Glu			co Gly					Ala	Gln
271 272	Arg Phe		Leu Se	er Val	Ser Val				Pro	His
273 274	Gln Val 2050							Lys Val	Glu	Thr
275 276	Lys Leu 2065	Lys Ala		ne Ser			g Tyr	Glu Glu 208		Arg
277 278	Ile Asp	Ala Arg	Gln Pr							Ile
279 280	Ile Thr					Gly Pro		Asn Ala	Leu	Ser
281 282	Lys Thr		Phe Gl		Arg Thr	Leu Ala			Gly	Tyr
283 284	Leu Ala 2130		_			Ala Lys		Val Ala	Ala	Pro
285	Gly Glu	Asn Ser			Ile Gln		a Arg	Pro Pro	Arg	Ala

Input Set: N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

286		2145	5			21	50			2.	155				216	0		
287		Asp	Ala	Thr	His	Arg	Ala	Pro	Arg	Ala	Asp	Glu	Pro	Ile	Ala	Val	Ile	
288		_			2	165				2170	_			217	5			
289		Glv	Met.	Ser	Glv	Ara	Tvr	Pro	Glv	Ala	Glu	Asn	Leu	Thr	Glu	Phe	grT	
290		- -1			180	5	-1-		218					190			_	
291		Glu	Δra			Δra	Glv	Δen			Tle	Thr			Pro	Pro	Glu	
292		GIU	-	2195	361	ALG	GLY	220		Cys	110		205	110	110	110	Olu	
		3			.	3	01				Desc			т	mi a	7 J -	7.1.	
293		-	_	ser	Leu	ASP	_		Pne	TAL	Pro	-	-	гуѕ	HIS	Ala	Ala	
294			2210				223					222						
295		Ala	Arg	Gly	Met			Ser	Lys			Gly	Phe	Leu		Gly	Phe	
296		2225				223					2235				22			
297		Ala	Asp	Phe	Asp	Pro	Leu	Phe	Phe	Asn	Ile	Ser	Pro	Arg	Glu	Ala	Thr	
298						2245				2:	250			:	2255			
299		Ser	Met	Asp	Pro	Gln	Glu	Arq	Leu	Phe	Leu	Gln	Ser	Cys	Trp	Glu	Val	
300				_	2260			,	22					227	_			
301		T.Au	Glu			Glv	Tyr	Thr			Ser	T.eu	Δla			Phe	Glv	
302		Бец		2275	AIU	GLY	1 7 1	2280		пор	DCI		285	0111	2129	1 110	011	
		Com			C1	1701	Dho			T10	mh x			C1 11	Trans.	Clu	T 011	
303				Val	СТА	vaı			GTĀ	ire			TIIT	СТУ	тут	Glu	ьеu	
304			2290			_	2295	-	_	_	230			_	_	_	1	
305				Ala	GLu			GТЪ	Arg			Ser	Val	Arg		Tyr	Thr	
306		2305				23:					2315				232	-		
307		Ser	Phe	Ala	Ser	Val	Ala	Asn	Arg	Val	Ser	${ t Tyr}$	Leu	Leu	Asp	Leu	Lys	
308					23	325				2330)			:	2335			
309		Gly	Pro	Ser	Met	Pro	Val	Asp	Thr	Met	Cys	Ser	Ala	Ser	Leu	Thr	Ala	
310		_		23	340				234	5			2	2350				
311		Val	His	Met	Ala	Cvs	Glu	Ala	Leu	Gln	Arq	Gly	Ala	Cys	Val	Met	Ala	
312				355		- 4 -		2360		-	,		365	-				
313		Tla			G1 v	Va 1	Δen			Val	His			Ser	Tvr	Val	Ser	
314			370	OI J	OI1	val	2375		-1-	,	238		001	501	- 1 -	,	501	
				C1	C1 n	Cln			C0.		250	50						
315				GTA	GTII		Met	ьеи	ser									
316	010	2385			_	239	3 U											
	<210>																	
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451			LVS	Va 1	Pro	Asp	Va 1	Lvs	Leu	Gln	Asp	Gln	Asp	Tle	Lvs	Val	Pro	
452		- I	-10		20	r	,	-10	25		P		_	30	-1-			
		T 011	λ l ¬			Th.∽	Dha	Thr		Clu	Tvc	Tlo		-	Dro	Lys	Len	
453		ьeu	AId		GTÀ	1111				Gru	пÃ2		ьец 15	FIO	FIO	пуз	ьeu	Λ
454		- 1		35		-		. 40		D 1	a 2			01	a 1	. 7 -	0	18
455		Ala		His	GLY	Phe			ser	Pne	Glu		Thr	GLY	GLu	Ala	ser	-
456			50				55					60					_	
457		Ile	Arg	Asn	Phe	Asn	Ser	Leu	Gly	Asp	Val	Asp	Glu	Asn	Gly	Ile	Ile	1
158				,		70	1				75				87)		•

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75

Gly Glu Pro Ser Pro Glu Ser Ala Glu Pro Gly Pro Arg Pro Gln Leu

Leu Leu Gly Ser Asp Ile Gly Trp Met Arg Tyr Gln Val Ser Ala Arg

458

459

460 461

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

	·		
462	. 100	105	110
463	Val Lys Ala Ala Val	Ser Ala Ser Leu Ser	Phe Leu Ala Ser Glu Asn
464	115	120	125
465	Gln Thr Glu Leu Ser	Val Thr Leu Ser Asp	Tyr Arg Ala His Pro Leu
466	130		L40
467	Gly Gln Asn Met Arg	Glu Ala Val Arg Ser	Asp Leu Ser Glu Leu Arg
468	145 15	50 155	160
469	Leu Met Gln Ala Thr	Asp Leu Ala Lys Leu	Thr Thr Gly Asp Ala Val
470	165	170	175
471	Ala Trp His Val Arg	Gly Ala Leu His Thr	Arg Leu Glu Leu Asn Trp
472	180	185	190
473	Ala Asp Ile Phe Pro	Thr Asn Leu Asn Arg	Leu Gly Phe Leu Arg Gly
474	195	200	205
475	Asn Glu Leu Leu Ala	Leu Lys Thr Ser Ala	Lys Ala Gly Leu Ser Ala
476	210	215	220
477	Arg Val Ser Leu Thr	Asp Asp Tyr Gln Leu	Ser Phe Ser Arg Pro Arg
478	225 23		240
479			Val Lys Ser His Glu Gln
480	245	250	255
481		Leu Glv Ile Thr Val	Glu Leu Leu Asp Pro Ala
482	260	265	270
483		- · ·	Glu Ala Leu Leu Gly Pro
484	275	280	285
485			Thr Ala Val Glu Ile Met
486	290		300
487			Lys Leu Asp Asp Asn Gln
488	305 31 Bed Val 115p		320
489			Leu Gly Ile Asp Pro Gln
490	325	330	335
491			Trp Ala Asp Phe Lys Ala
492	340	345	350
493			Arg Thr Gln Val Ala Glu
494	355	360	365
495			Glu Thr Ser Thr Leu Leu
496	370	375	380
497		= : :	Arg Phe His Glu Ser Leu
498	385 390	_	400
499		. -	Trp Met Lys Ser Leu Pro 415
500	405	All Tou Ama Agn	
501		425	Tyr Leu His Ala Thr Thr 430
502	420		
503		-	Leu Gly Leu Gly Ser Phe
504	435	440	445
505	-	-	Gln Ser Trp Val Thr Gln
506	450	455	460
507	-		Phe Leu Gly Arg Arg Gly
508	465 47		480
509			Gln Trp Val Val Asp Leu
510	485	490	495

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

10																			
Gly Tyr Gly Leu His Leu Met Leu Trp Gly Arg Gln Lys Lys Leu Ser			Lys	Ala	_		Thr	Arg	Phe			Thr	Pro			Ser	Asp	Phe	
514 515 520 525 515 Arg Lys Asp Leu Gln Gln Ala Val Asp Asp Ala Val Val Trp Gly Val 516 530 535 535 540 517 Leu Asp Ala Lys Asp Ala Ala Thr Val Ile Ser Thr Met Gln Glu Asp 518 545 550 555 560 519 Met Gly Lys His Pro Ile Glu Thr Arg Leu Glu Leu Lys Met Ala Asp 520 565 570 570 575 580 585 590 582 Asp Ser Phe Arg Ala Leu Val Pro Arg Ile Gln Thr Leu Glu Leu Ser 522 580 585 590 523 Arg Phe Ser Arg Ala Leu Ala Arg Ala Leu Pro Trp Ser Glu Gln Leu 524 595 600 605 525 Pro Arg Ala Ser Ala Glu Phe Arg Arg Ala Leu Tyr Ala Pro Ile Trp 526 610 615 527 Glu Ala Tyr Leu Arg Glu Val Gln Glu Gln Gly Ser Leu Met Leu Asn 528 625 630 635 665 529 Asp Leu Ser Pro Ser Arg Ala Ala Gln Ile Ala Lys Trp Tyr Phe Gln 530 645 650 650 531 Lys Asp Pro Thr Val Arg Asp Leu Gly Lys Asp Leu Gln Leu Ile Glu 532 660 665 533 Ser Glu Trp Arg Pro Gly Gly Gly Asn Phe Ser Phe Ala Glu Val Ile 534 675 680 685 535 Ser Lys Asn Pro Asn Thr Leu Met Arg Cys Arg Asn Phe Val Ser Gly 536 690 695 700 537 Met Val Arg Leu Arg Arg Ala Ile Asp Glu Arg Lys Ala Pro Asp Glu 538 705 710 725 730 735 541 His Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr 542 740 745 750 780 543 Pro Leu Gly Leu Ala Gly Val Glu Leu Gly Met Trp Thr Thr Gly Phe 544 755 760 765 545 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 548 785 550 <210> SEQ ID NO: 4 551 <211> LEURGH: 529 552 <212> TYPE: Amino acid 558 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 725 730 557 558 Cln NGANISM: Myxococcus xanthus 554 (400) SEQUENCE: 4 559 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 559 Callo Sec Gln No: 4 550 Cln Sec Gln No: 4 550 Cln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 550 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 559 Callo Sec Gln No: 4 550 Cln Sec Gln Not Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu			_										_			_	_	_	
Arg Lys Asp Leu Gln Gln Ala Val Asp Asp Ala Val Val Trp Gly Val 510 530 535 540 540 540 545 550 555 560 550 570 575 575 521 Asp Ser Phe Arg Ala Leu Val Pro Arg Ile Gln Thr Leu Glu Leu Ser 580 580 585 590 570 575 575 521 Asp Ser Phe Arg Ala Leu Ala Arg Ala Leu Pro Trp Ser Glu Gln Leu Ser 580 580 585 590 605 585 590 605 585 590 605 655 590 605 585 590 605 655 590 605 605 605 605 605 605 605 605 605 60	513		Gly	Tyr	Gly	Leu	His	Leu			Trp	СТÄ	_		Lys	Lys	Leu	Ser	
516	514																		
Leu Asp Ala Lys Asp Ala Ala Thr Val Ile Ser Thr Met Gln Glu Asp 518 545 550 550 555 560 555 560 555 560 570 575 570 575 575 570 575 575 570 575 575	515		Arg	Lys	Asp	Leu	Gln	Gln	Ala	Val	Asp	Asp	Ala	Val	Val	${\tt Trp}$	Gly	Val	
518 545 550 555 560 519 Met Gly Lys His Pro Ile Glu Thr Arg Leu Glu Leu Lys Met Ala Asp 520 555 570 575 521 Asp Ser Phe Arg Ala Leu Val Pro Arg Ile Gln Thr Leu Glu Leu Ser 580 585 590 585 523 Arg Phe Ser Arg Ala Leu Ala Arg Ala Leu Pro Trp Ser Glu Gln Leu 595 600 605 524 595 600 605 525 Pro Arg Ala Ser Ala Glu Phe Arg Ala Leu Pro Trp Ser Glu Gln Leu 595 600 605 526 Glu Ala Tyr Leu Arg Glu Val Gln Glu Gln Gly Ser Leu Met Leu Asn 615 620 527 Glu Ala Tyr Leu Arg Glu Val Gln Glu Gln Gly Ser Leu Met Leu Asn 625 625 528 625 630 635 640 529 Asp Leu Ser Pro Ser Arg Ala Ala Gln Ile Ala Lys Trp Tyr Phe Gln 645 650 655 531 Lys Asp Pro Thr Val Arg Asp Leu Gly Lys Asp Leu Gln Leu Ile Glu 670 532 660 665 655 533 Ser Glu Trp Arg Pro Gly Gly Gly Asn Phe Ser Phe Ala Glu Val Ile 675 680 685 535 Ser Lys Asn Pro Asn Thr Leu Met Arg Cys Arg Asn Phe Val Ser Gly 690 695 700 536 690 695 710 715 720 537 Met Val Arg Leu Arg Arg Ala Ile Asp Glu Arg Lys Ala Pro Asp Glu 705 720 735 541 His Leu Arg Ala Ala Gly Ser Leu Leu Glu Gly Met Trp Thr Thr Gly Phe 725 730 735 542 740 745 750 765 543 Pro Leu Gly Leu Ala Gly Val Glu Arg Thr Leu Ala Gln Ser Thr 614 Asp Ser Glu	516			530				5	35				540						
Met Gly Lys His Pro Ile Glu Thr Arg Leu Glu Leu Lys Met Ala Asp 560 565 570 575	517		Leu	Asp	Ala	Lys	Asp	Ala	Ala	Thr	Val	Ile	Ser	Thr	Met	Gln	Glu	Asp	
Second	518		545	-		_	5	50				555				560)		
Second			Met	Glv	Lvs	His	Pro	Ile	Glu	Thr	Arg	Leu	Glu	Leu	Lys	Met	Ala	Asp	
Asp Ser Phe Arg Ala Leu Val Pro Arg Ile Gln Thr Leu Glu Leu Ser 580 580 590 Arg Phe Ser Arg Ala Leu Ala Arg Ala Leu Pro Trp Ser Glu Gln Leu 595 600 605 Dro Arg Ala Ser Ala Glu Phe Arg Arg Ala Val Tyr Ala Pro Ile Trp 610 615 620 Glu Ala Tyr Leu Arg Glu Val Gln Glu Gln Gly Ser Leu Met Leu Asn 625 625 630 635 640 Asp Leu Ser Pro Ser Arg Ala Ala Gln Ile Ala Lys Trp Tyr Phe Gln 645 650 655 Lys Asp Pro Thr Val Arg Asp Leu Gly Lys Asp Leu Gln Leu Ile Glu 665 650 Ser Lys Asp Pro Thr Val Arg Asp Leu Gly Lys Asp Leu Gln Leu Ile Glu 675 680 665 Ser Lys Asn Pro Asn Thr Leu Met Arg Cys Arg Asn Phe Val Ser Gly 690 695 700 Met Val Arg Leu Arg Arg Ala Ile Asp Glu Arg Lys Ala Pro Asp Glu 705 720 Leu Arg Thr Val Phe Gly Glu Leu Glu Gly Met Trp Thr Thr Gly Phe 725 730 735 Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr 740 740 745 750 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 785 Asp Ser Glu Gln Leu Ala Gly Val Glu Arg Thr Leu Thr Val Arg Val Ala 755 760 775 780 Asp Ser Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 785 Asp Ser Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 785 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 785 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 785 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 785 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 785 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 785 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 785 Asp Ser Glu Glu Gln Leu Val Phe Ser Asp Leu Ala Phe Val Leu Pro Pro 156 1 5 10 15 Het Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 156 1 5 10 15 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 20 25				_	-						-							_	
S22 S80 S85 S90 S95 S90 S93 Arg Phe Ser Arg Ala Leu Ala Arg Ala Leu Pro Trp Ser Glu Gln Leu S24 S95 600 605 605 605 605 600 605 605 600 605 600 605 600 605 600 605 600 605 600 605 600 605 620 610 615 620 620 625 630 635 640 635 640 645 630 635 640 665 650 665 650 665 665 665 665 665 665 665 665 665 665 665 665 665 660 665 665 660 665			Asp	Ser	Phe	Ara	Ala	Leu	Va 1	Pro	Ara	Ile	Gln	Thr	Leu	Glu	Leu	Ser	
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524 595 600 605			λνα	Dho			Δla	T.A.II	Δla			T.011	Pro			Glu	Gln	Leu	
Pro Arg Ala Ser Ala Glu Phe Arg Arg Ala Val Tyr Ala Pro Ile Tro 610 615 620 610 615 620 615 620 615 620 615 620 615 620 615 620 610 Glu Ala Tyr Leu Arg Glu Val Gln Glu Gln Gly Ser Leu Met Leu Asn 625 630 625 630 635 640 640 655 650 650 655 640 655 650 655 655 645 650 655 655 650 655 655 655 655 650 655 655			лту			ALG	AIG	Leu			niu	пса			001	Olu	0111	пса	
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Signature Sig					Ата	ser	АТА			Arg	Ary			тут	нта	PIO	TTE	тъ	
528 625 630 635 640 529 Asp Leu Ser Pro Ser Arg Ala Ala Gln Ile Ala Lys Trp Tyr Phe Gln 530 645 650 655 531 Lys Asp Pro Thr Val Arg Asp Leu Gly Lys Asp Leu Gln Leu Ile Glu 532 660 665 670 533 Ser Glu Trp Arg Pro Gly Gly Gly Asn Phe Ser Phe Ala Glu Val Ile 534 675 680 685 535 Ser Lys Asn Pro Asn Thr Leu Met Arg Cys Arg Asn Phe Val Ser Gly 536 690 695 700 537 Met Val Arg Leu Arg Arg Ala Ile Asp Glu Arg Lys Ala Pro Asp Glu 538 705 710 720 539 Leu Arg Thr Val Phe Gly Glu Leu Glu Gly Met Trp Thr Thr Gly Phe 540 725 730 735 541 His Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr 542 740 745 750 543 Pro Leu Gly Leu Ala Gly Val Glu Arg Thr Leu Thr Val Arg Val Ala 544 755 760 765 545 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 546 770 775 780 557 Ala 558 785 550 <210> SEQ ID NO: 4 551 <211> LENGTH: 529 552 <212> TYPE: Amino acid PKT 553 <213> ORGANISM: Myxococcus xanthus 554 (400) SEQUENCE: 4 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 556 1 5 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 20 25 30					_	_				a 1	a1			a	T	14-4	T	3	
Asp Leu Ser Pro Ser Arg Ala Ala Gln Ile Ala Lys Trp Tyr Phe Gln 645 645 665 650 651 1 Lys Asp Pro Thr Val Arg Asp Leu Gly Lys Asp Leu Gln Leu Ile Glu 660 665 670 533 Ser Glu Trp Arg Pro Gly Gly Gly Asn Phe Ser Phe Ala Glu Val Ile 675 680 685 535 Ser Lys Asn Pro Asn Thr Leu Met Arg Cys Arg Asn Phe Val Ser Gly 690 695 700 537 Met Val Arg Leu Arg Arg Ala Ile Asp Glu Arg Lys Ala Pro Asp Glu 538 705 710 715 720 539 Leu Arg Thr Val Phe Gly Glu Leu Glu Gly Met Trp Thr Thr Gly Phe 725 730 735 541 His Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr 542 740 745 750 543 Pro Leu Gly Leu Ala Gly Val Glu Arg Thr Leu Thr Val Arg Val Ala 644 755 760 765 545 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 746 747 Ala 748 748 750 550 <210> SEQ ID NO: 4 551				Ala	Tyr	Leu			vaı	GIN			GTA	ser	Leu			ASII	
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Lys Asp Pro Thr Val Arg Asp Leu Gly Lys Asp Leu Gln Leu Ile Glu 660 665 670 670 670 660 665 670 670 670 670 670 670 670 670 670 670			Asp	Leu	Ser			Arg	Ala	Ala		IIe	Ala	Lys			Phe	GIn	
Ser Glu Trp Arg Pro Gly Gly Gly Asn Phe Ser Phe Ala Glu Val Ile 675 680 685 685 686 685 686 685 686 685 686 685 686 685 686 687 686 687 688 688 688 688 689 690 695 700 688 689 690 695 700 688 689 690 695 700 688 689 690 695 700 688 689 700 688 689 700 688 689 700 688 689 700 688 689 700 688 689 700 700 715 700 715 720 720 720 735 730 735 641 His Leu Arg Ala Phe Gly Glu Leu Glu Gly Met Trp Thr Thr Gly Phe 725 730 735 741 His Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr 642 740 745 750 765 743 Pro Leu Gly Leu Ala Gly Val Glu Arg Thr Leu Thr Val Arg Val Ala 644 755 760 765 645 648 785 650 6210> SEQ ID NO: 4 6551 6512 6522 653 653 6540 685 685 685 685 685 685 685 685 685 685																			
Ser Glu Trp Arg Pro Gly Gly Gly Asn Phe Ser Phe Ala Glu Val Ile 675 680 685 685 686 685 686 687 690 690 695 700 690 700 690 700 715 720 720 733 Met Val Arg Leu Arg Arg Ala Ile Asp Glu Arg Lys Ala Pro Asp Glu 705 705 705 706 707 707 707 707 707 707 707 707 707	531		Lys	Asp	Pro	Thr	Val	Arg	Asp	Leu	Gly	Lys	Asp	Leu	Gln	Leu	Ile	Glu	
534 535 Ser Lys Asn Pro Asn Thr Leu Met Arg Cys Arg Asn Phe Val Ser Gly 536 690 695 700 537 Met Val Arg Leu Arg Arg Ala Ile Asp Glu Arg Lys Ala Pro Asp Glu 538 705 710 715 720 539 Leu Arg Thr Val Phe Gly Glu Leu Glu Gly Met Trp Thr Thr Gly Phe 725 730 735 541 His Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr 542 740 745 750 765 760 765 765 Asp Ser Glu Glu Glu Glu Arg Thr Leu Thr Val Arg Val Ala 755 760 76	532																		
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536 690 695 700 537 Met Val Arg Leu Arg Arg Ala Ile Asp Glu Arg Lys Ala Pro Asp Glu 538 705 710 715 720 539 Leu Arg Thr Val Phe Gly Glu Leu Glu Gly Met Trp Thr Thr Gly Phe 725 730 735 541 His Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr 542 740 745 750 543 Pro Leu Gly Leu Ala Gly Val Glu Arg Thr Leu Thr Val Arg Val Ala 544 755 760 765 545 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 546 770 775 780 547 Ala 548 785 550 <210> SEQ ID NO: 4 551 <211> LENGTH: 529 552 <212> TYPE: Amino acid	534				675				680)			(685					
Met Val Arg Leu Arg Arg Ala Ile Asp Glu Arg Lys Ala Pro Asp Glu 538 705 710 715 720	535		Ser	Lys	Asn	Pro	Asn	Thr	Leu	Met	Arg	Cys	Arg	Asn	Phe	Val	Ser	Gly	
The first state The first	536		6	690				6	95				700)					•
The first state The first	537		Met	Val	Arg	Leu	Arq	Arq	Ala	Ile	Asp	Glu	Arq	Lys	Ala	Pro	Asp	Glu	
Leu Arg Thr Val Phe Gly Glu Leu Glu Gly Met Trp Thr Thr Gly Phe 725 730 735 541 His Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr 740 745 750 543 Pro Leu Gly Leu Ala Gly Val Glu Arg Thr Leu Thr Val Arg Val Ala 755 760 765 545 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 770 775 780 547 Ala 548 785 550 <210> SEQ ID NO: 4 551 <211> LENGTH: 529 552 <212> TYPE: Amino acid PKT 553 <213> ORGANISM: Myxococcus xanthus 554 <400> SEQUENCE: 4 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 556 1 5 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 30	538				_		_	_			_		-	_					
540 725 730 735 741 His Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr 542 740 745 750 543 Pro Leu Gly Leu Ala Gly Val Glu Arg Thr Leu Thr Val Arg Val Ala 544 755 760 765 545 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 546 770 775 780 547 Ala 548 785 550 <210> SEQ ID NO: 4 551 <211> LENGTH: 529 552 <212> TYPE: Amino acid PRT 553 <213> ORGANISM: Myxococcus xanthus 554 <400> SEQUENCE: 4 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 556 1 5 10 15 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 20 25 30				Ara	Thr	Val	Phe	Glv	Glu	Leu	Glu	Glv	Met	Trp	Thr	Thr	Gly	Phe	
His Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr 740 745 750 750 750 745 750 750 765 760 765 765 760 765 765 760 765 765 760 765 765 760 765 765 760 765 765 760 760 765 760 760 765 760 765 760 760 760 760 760 760 760 765 760 760 760 760 760 760 760 760 760 760				9				2						_			-		
740 745 750 750 7543 Pro Leu Gly Leu Ala Gly Val Glu Arg Thr Leu Thr Val Arg Val Ala 755 760 765 765 760 765 766 780 780 780 780 780 780 780 780 780 780			His	Len	Ara			Glv	Ser	Leu		-	Asp	Leu	Ala	Gln	Ser	Thr	
Pro Leu Gly Leu Ala Gly Val Glu Arg Thr Leu Thr Val Arg Val Ala 755 760 765 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 770 775 780 Ala 785 548 785 550 <210> SEQ ID NO: 4 551 <211> LENGTH: 529 552 <212> TYPE: Amino acid PR 553 <213> ORGANISM: Myxococcus xanthus 554 <400> SEQUENCE: 4 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 556 1 5 10 15 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 10 10 25 30				Dou	_			011	201				E						
544 755 760 765 545 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 546 770 775 780 547 Ala 548 785 550 <210> SEQ ID NO: 4 551 <211> LENGTH: 529 552 <212> TYPE: Amino acid PRT 553 <213> ORGANISM: Myxococcus xanthus 554 <400> SEQUENCE: 4 555 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 556 1 5 10 15 557 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 20 25 30			Dro	LOU			λla	G1v	Va 1		Δra	Thr	T.011			Δra	Val	Δla	
Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala 770 775 780 Ala 785 547 Ala 785 550 <210> SEQ ID NO: 4 551 <211> LENGTH: 529 552 <212> TYPE: Amino acid PRT 553 <213> ORGANISM: Myxococcus xanthus 554 <400> SEQUENCE: 4 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 1 5 10 15 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 25 30			FIO		_	пец	пла	GLY			ni 9	1111			, 441	1119	· u ·	2114	
546 770 775 780 547 Ala 548 785 550 <210> SEQ ID NO: 4 551 <211> LENGTH: 529 552 <212> TYPE: Amino acid PRT 553 <213> ORGANISM: Myxococcus xanthus 554 <400> SEQUENCE: 4 555 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 556 1 5 10 15 557 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 25 30			7.00			C1.,	Cln	Tou			Cor	Thr			Sar	Thr	Glv	λla	
547 Ala 548 785 550 <210> SEQ ID NO: 4 551 <211> LENGTH: 529 552 <212> TYPE: Amino acid PRT 553 <213> ORGANISM: Myxococcus xanthus 554 <400> SEQUENCE: 4 555 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 556 1 5 10 15 557 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 25 30			ASP		GIU	GIU	GIII			FIIE	Ser	1111		AIG	261	TIIL	Gry	нια	
548 785 550 <210> SEQ ID NO: 4 551 <211> LENGTH: 529 552 <212> TYPE: Amino acid PRT 553 <213> ORGANISM: Myxococcus xanthus 554 <400> SEQUENCE: 4 555 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 556 1 5 10 15 557 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 25 30				//0				/	/ 3				700						
550 <210> SEQ ID NO: 4 551 <211> LENGTH: 529 552 <212> TYPE: Amino acid PRT 553 <213> ORGANISM: Myxococcus xanthus 554 <400> SEQUENCE: 4 555																			
551 <211> LENGTH: 529 552 <212> TYPE: Amino acid PRT 553 <213> ORGANISM: Myxococcus xanthus 554 <400> SEQUENCE: 4 555						_													
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554 <400> SEQUENCE: 4 555 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 556 1 5 10 15 557 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 25 30								/K']											
555 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro 556 1 5 10 15 557 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 25 30	553	<213>	ORG	ANIŜĪ	M: My	yxoco	occus	s xaı	nthus	5									
556 1 5 10 15 557 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 25 30	554	<400>																	
556 1 5 10 15 557 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu 558 20 25 30	555		Met	Pro	Ser	Gly	Cys	Tyr	Gly	Ala	Ala	Ser	Ala	Phe	Val	Leu	Pro	Pro	
558 20 25 30	556		_			5	5												
558 20 25 30			Leu	Pro	Ala	Met	Pro	Gln	Ala	Pro	Ser	Asp	Val	Ser	Gln	Val	Leu	Leu	
												-							
			Pro	Phe	Gly	Gly	Leu	Val	Gly	Arg	Glu	Val	Asp	Leu	Asp	Ala	Phe	Leu	_

40

45

some

same

35

EO/E>

560

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/710,262D

DATE: 10/21/2002
TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

561	Gln Thr Leu Met Asp Arg Ile Ala Ile Thr Leu	ı Gln Ala Asp Arg Gly
562	50 55 60	
563	Thr Leu Trp Leu Leu Asp Pro Ala Arg Arg Glu	
564	65 70 75	80
565	Ala His Leu Pro Glu Val Ser Gln Ile Arg Val	
566	85 90	95
567	Val Ala Gly Thr Val Ala Lys Ala Gly His Ala	
568	100 105	110
569	Pro Arg Gly Glu Gln Arg Phe Phe Ala Asp Ile	125
570	115 120 Tyr Arg Thr Thr Ser Leu Leu Ala Val Pro Leu	
571	130 135 140	t Aig Asp Giy Asp Giy
572	Ala Leu Tyr Gly Val Leu Gln Val Leu Asn Arg	Ara Cly Clu Aen Ara
573 574	145 150 155	160
57 4 575	Phe Thr Asp Glu Asp Thr Gln Arg Leu Thr Ala	— · ·
576	165 170	175
577	Ser Thr Ala Leu Gln Ser Thr Ser Leu Tyr Glr	
578	180 185	190
579	Lys Glu Gln Pro Gln Val Pro Val Gly Tyr Phe	— - ·
580	195 200	205
581	Gly Glu Ser Pro Gln Leu Gln Ala Ile Tyr Arg	
582	210 215 220	,
583	Ala Pro Thr Asp Ala Thr Val Leu Leu Arg Gly	Glu Ser Gly Ser Gly
584	225 230 235	240
585	Lys Glu Leu Phe Ala Arg Ala Val His Val Asr	Gly Pro Arg Arg Asp
586	245 250	255
587	Gln Pro Phe Ile Lys Val Asp Cys Ala Ala Leu	Pro Ala Thr Leu Ile
588	260 265	270
589	Glu Asn Glu Leu Phe Gly His Glu Arg Gly Ala	Phe Thr Gly Ala Asp
590	275 280	285
591	His Arg Val Pro Gly Lys Phe Glu Ala Ala Ser	: Gly Gly Thr Val Phe
592	290 . 295 . 300	
593	Ile Asp Glu Ile Gly Glu Leu Pro Leu Pro Val	
594	305 310 315	320
595	Arg Val Ile Gln Asp Arg Glu Phe Glu Arg Val	
596	325 330	335
597	Val Lys Val Asp Val Arg Ile Val Ala Ala Thr	
598	340 345	350
599	Arg Met Val Ala Glu Gly Arg Phe Arg Glu Asp	365
600	355 360 Lys Val Val Glu Val Val Leu Pro Pro Leu Arg	
601 602		, Gid Alg Gly Ala Gid
603	370 375 380 Asp Ile Glu Arg Leu Ala Arg His Phe Val Ala	a Ala Val Ala Arg Arg
604	385 390 395	400
605	His Arg Leu Thr Pro Pro Arg Leu Ser Ala Ala	
606	405 410	415
607	Lys Arg Tyr Arg Trp Pro Gly Asn Val Arg Glu	
608	420 425	430
609	Glu Ser Ala Val Val Leu Cys Glu Gly Glu Ile	

Input Set: N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
610
                                        440
              Pro Leu Pro Asp Val Asp Arg Ala Ala Leu Pro Pro Ala Ala Ala
    611
                                     455
                                            .
    612
              Gln Gly Val Asn Ala Pro Thr Ala Pro Ala Pro Leu Asp Ala Gly Leu
    613
                                470
                                                  475
    614
              Leu Pro Leu Ala Glu Val Glu Arg Arg His Ile Leu Arg Val Leu Asp
    615
                                               490
    616
              Ala Val Lys Gly Asn Arg Thr Ala Ala Ala Arg Val Leu Ala Ile Gly
    617
    618
                                           505
                                                             510
              Arg Asn Thr Leu Ala Arg Lys Leu Lys Glu Tyr Gly Leu Gly Asp Glu
    619
    620
                                        520
    621
              Pro
    623 <210> SEQ ID NO: 5
    624 <211> LENGTH; 292
    625 <212> TYPE: (Amino acid ) PRT
    626 <213> ORGANISM: Myxococcus xanthus
\partial H-> 627 <400> SEQUENCE: 5
              Met Arg Ala Ser Gln Ala Glu Ala Pro His Ser Arg Arg Leu Thr Met
    628
    629
                                                10
    630
              Glu Val Arg Phe His Gly Val Arg Gly Ser Ile Ala Val Ser Gly Ser
    631
    632
              Arg Ile Gly Gly Asn Thr Ala Cys Val Glu Val Thr Ser Gln Gly His
    633
    634
              Arg Leu Ile Leu Asp Ala Gly Thr Gly Ile Arg Ala Leu Gly Glu Ile
    635
                                     55
                                                      60
              Met Met Arg Glu Gly Ala Pro Gln Glu Ala Thr Leu Phe Phe Ser His
    636
    637
                                  70
                                                   75
              Leu His Trp Asp His Val Gln Gly Phe Pro Phe Phe Thr Pro Ala Trp
    638
                              85
                                                90
    639
              Leu Pro Thr Ser Glu Leu Thr Leu Tyr Gly Pro Gly Ala Asn Gly, Ala
    640
    641
                                            105
              Gln Ala Leu Gln Ser Glu Leu Ala Ala Gln Met Gln Pro Leu His Phe
    642
                                                           125
    643
                                        120
              Pro Val Pro Leu Ser Thr Met Arg Ser Arg Met Asp Phe Arg Ser Ala
    644
    645
                                                        140
                                    135
              Leu His Ala Arg Pro Val Glu Val Gly Pro Phe Arg Val Thr Pro Ile
    646
    647
                                150
                                                  155
                                                                    160
    648
              Asp Val Pro His Pro Gln Gly Cys Leu Ala Tyr Arg Leu Glu Ala Asp
    649
                             165
                                                170
    650
              Gly His Ser Phe Val Tyr Ala Thr Asp Val Glu Val Arg Val Gln Glu
    651
                                           185
                                                              190
    652
              Leu Ala Pro Glu Val Gly Arg Leu Phe Glu Gly Ala Asp Val Leu Cys
    653
                                        200
              Leu Asp Ala Gln Tyr Thr Pro Asp Glu Tyr Glu Gly Arg Lys Gly Val
    654
    655
                                    215
                                                        220
              Ala Lys Lys Gly Trp Gly His Ser Thr Met Met Asp Ala Ala Gly Val
    656
                                                  235
    657
                                 230
              Ala Gly Leu Val Gly Ala Arg Arg Leu Cys Leu Phe His His Asp Pro
    658
    659
                                               250
```

DATE: 10/21/2002

PATENT APPLICATION: US/09/710,262D TIME: 16:29:22 Input Set : N:\Crf4\10182002\I710262D.raw Output Set: N:\CRF4\10212002\I710262D.raw Ala His Gly Asp Asp Met Leu Glu Asp Met Ala Glu Gln Ala Arg Ala Leu Phe Pro Val Cys Glu Pro Ala Arg Glu Gly Gln Arg Leu Val Leu Gly Arg Ala Ala 667 <210> SEQ ID NO: 6 668 <211> LENGTH: 168 669 <212> TYPE: Amino acid 670 <213> ORGANISM: Myxococcus xanthus 24/2> 671 <400> SEQUENCE: 6 Met Pro Gly Pro Arg Cys Ala Glu Asn Asp Trp Val Ala Leu Leu Val Arg Val Asn His Glu Lys Val Ala Ala Ala Gln Leu Gly Lys His Gly Tyr Glu Phe Phe Leu Pro Thr Tyr Thr Pro Pro Lys Ser Ser Gly Val Lys Ala Lys Leu Pro Leu Phe Pro Gly Tyr Leu Phe Cys Arg Tyr Gln Same Pro Leu Asn Pro Tyr Arg Ile Val Arg Ala Pro Gly Val Ile Arg Leu Leu Gly Gly Asp Ala Gly Pro Glu Ala Val Pro Ala Gln Glu Leu Glu Ala Ile Arg Arg Val Ala Asp Ser Gly Val Ser Ser Asn Pro Cys Asp Tyr Leu Arg Val Gly Gln Arg Val Arg Ile Ile Glu Gly Pro Leu Thr Gly Leu Glu Gly Ser Leu Val Thr Ser Lys Ser Gln Leu Arg Phe Ile Val Ser Val Gly Leu Leu Gln Arg Ser Val Ser Val Glu Val Ser Ala Glu Gln Leu Glu Pro Ile Thr Asp 695 <210> SEQ ID NO: 7 696 <211> LENGTH: 79 697 <212> TYPE Amino acid 698 <213> ORGANISM: Myxococcus xanthus > 699 <400> SEQUENCE: 7 Met Asp Lys Arg Ile Ile Phe Asp Ile Val Thr Ser Ser Val Arg Glu Val Val Pro Glu Leu Glu Ser His Pro Phe Glu Pro Glu Asp Asp Leu Val Gly Leu Gly Ala Asn Ser Leu Asp Arg Ala Glu Ile Val Asn Leu Thr Leu Glu Lys Leu Ala Leu Asn Ile Pro Arg Val Glu Leu Ile Asp Ala Lys Thr Ile Gly Gly Leu Val Asp Val Leu His Ala Arg Leu 711 <210> SEQ ID NO: 8

RAW SEQUENCE LISTING

DATE: 10/21/2002 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/710,262D TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw Output Set: N:\CRF4\10212002\I710262D.raw

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712 <211> LENGTH; 420
     713 <212> TYPE: (Amino acid )
     714 <213> ORGANISM: Myxococcus xanthus
(E)€-> 715 <400> SEQUENCE: 8
               Met Gly Pro Val Gly Ile Glu Ala Met Asn Ala Tyr Cys Gly Ile Ala
     717
                                               10
     718
               Arg Leu Asp Val Leu Gln Leu Ala Thr His Arg Gly Leu Asp Thr Ser
     719
                           20
                                              25
               Arg Phe Ala Asn Leu Leu Met Glu Glu Lys Thr Val Pro Leu Pro Tyr
     720
     721
                                          40
               Glu Asp Pro Val Thr Tyr Gly Val Asn Ala Ala Arg Pro Ile Leu Asp
     722
     723
                                     55
               Gln Leu Thr Ala Ala Glu Arg Asp Ser Ile Glu Leu Leu Val Ala Cys
     724
                                                   75
                                 70
     725
               Thr Glu Ser Ser Phe Asp Phe Gly Lys Ala Met Ser Thr Tyr Leu His
     726
     727
                                                  90
     728
               Gln His Leu Gly Leu Ser Arg Asn Cys Arg Leu Ile Glu Leu Lys Ser
     729
                                            105
                                                               110
               Ala Cys Tyr Ser Gly Val Ala Gly Leu Gln Met Ala Val Asn Phe Ile
     730
     731
                                       120
               Leu Ser Gly Val Ser Pro Gly Ala Lys Ala Leu Val Val Ala Ser Asp
     732
     733
                                    135
                                                       140
               Leu Ser Arg Phe Ser Ile Ala Glu Gly Gly Asp Ala Ser Thr Glu Asp
     734
     735
                                                  155
                                 150
               Trp Ser Phe Ala Glu Pro Ser Ser Gly Ala Gly Ala Val Ala Met Leu
     736
     737
                                               170
                                                                 175
               Val Ser Asp Thr Pro Arg Val Phe Arg Val Asp Val Gly Ala Asn Gly
     738
     739
                                            185
               Tyr Tyr Gly Tyr Glu Val Met Asp Thr Cys Arg Pro Val Ala Asp Ser
     740
     741
                                       200
     742
               Glu Ala Gly Asp Ala Asp Leu Ser Leu Leu Ser Tyr Leu Asp Cys Cys
     743
                                     215
                                                        220
               Glu Asn Ala Phe Arg Glu Tyr Thr Arg Arg Val Pro Ala Ala Asn Tyr
     744
                                                   235
     745
     746
               Ala Glu Ser Phe Gly Tyr Leu Ala Phe His Thr Pro Phe Gly Gly Met
                                                250
                                                                   255
     747
                              245
     748
               Val Lys Gly Ala His Arg Thr Met Met Arg Lys Phe Ser Gly Lys Asn
     749
                                           265
                         260
               Arg Gly Asp Ile Glu Ala Asp Phe Gln Arg Arg Val Ala Pro Gly Leu
     750
     751
                                        280
                                                          285
     752
               Thr Tyr Cys Gln Arg Val Gly Asn Ile Met Gly Ala Thr Met Ala Leu
     753
                                    295
                                                      300
               Ser Leu Leu Gly Thr Ile Asp His Gly Asp Phe Ala Thr Ala Lys Arg
     754
     755
                                                   315
     756
               Ile Gly Cys Phe Ser Tyr Gly Ser Gly Cys Ser Ser Glu Phe Phe Ser
     757
                                               330
     758
               Gly Val Val Thr Glu Glu Gly Gln Gln Arg Gln Arg Ala Leu Gly Leu
     759
                                           345
               Gly Glu Ala Leu Gly Arg Arg Gln Gln Leu Ser Met Pro Asp Tyr Asp
```

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
761
                                    360
          Ala Leu Leu Lys Gly Asn Gly Leu Val Arg Phe Gly Thr Arg Asn Ala
762
763
                                 375
764
          Glu Leu Asp Phe Gly Val Val Gly Ser Ile Arg Pro Gly Gly Trp Gly
765
                             390
                                              395
          Arg Pro Leu Leu Phe Leu Ser Ala Ile Arg Asp Phe His Arg Asp Tyr
766
                                           410
767
                          405
768
          Gln Trp Ile Ser
769
                     420
771 <210> SEQ ID NO: 9
772 <211> LENGTH: 325
773 <212> TYPE: Amino acid
774 <213> ORGANISM: Myxococcus xanthus
775 <400> SEQUENCE: 9
776
          Met Ser Ser Val Ala Thr Ala Val Pro Leu Thr Ala Arg Asp Ser Ala
777
                                           10
778
          Val Ser Arg Arg Leu Arg Ile Thr Pro Ser Met Cys Gly Gln Thr Ser
779
                                       25
780
          Leu Phe Ala Gly Gln Ile Gly Asp Trp Ala Trp Asp Thr Val Ser Arg
781
                                    40
782
          Leu Cys Gly Thr Asp Val Leu Thr Ala Thr Asn Ala Ser Gly Ala Pro
783
                                  55
          Thr Tyr Leu Ala Phe Tyr Tyr Phe Arg Ile Arg Gly Thr Pro Ala Leu
784
785
                             70
                                                75
786
          His Pro Gly Ala Leu Arg Phe Gly Asp Thr Leu Asp Val Thr Ser Lys
787
                                            90
                          85
788
          Ala Tyr Asn Phe Gly Ser Glu Ser Val Leu Thr Val His Arg Ile Cys
789
                                        105
790
          Lys Thr Ala Glu Gly Gly Ala Pro Glu Ala Asp Ala Phe Gly His Glu
791
                                                      125
                                   120
          Glu Leu Tyr Glu Gln Pro Gln Pro Gly Arg Ile Tyr Ala Glu Thr Phe
792
793
                                135
                                                 140
794
          Asn Arg Trp Ile Thr Arg Ser Asp Gly Lys Ser Asn Glu Ser Leu Ile
795
                           150
                                              155
796
          Lys Ser Ser Pro Val Gly Phe Gln Tyr Ala His Leu Pro Leu Leu Pro
797
                                           170
          Asp Glu Tyr Ser Pro Arg Arg Ala Tyr Gly Asp Ala Arg Ala Arg Gly
798
799
                                       185
                                                          190
800
          Thr Phe His Asp Val Asp Ser Ala Glu Tyr Arg Leu Thr Val Asp Arg
801
                                     200
802
          Phe Pro Leu Arg Tyr Ala Val Asp Val Ile Arg Asp Val Asn Gly Val
803
                                 215
                                                  220
          Gly Leu Ile Tyr Phe Ala Ser Tyr Phe Ser Met Val Asp Trp Ala Ile
804
805
                           230
                                              235
                                                                 240
          Trp Gln Leu Ala Arg His Gln Gly Arg Ser Glu Gln Ala Phe Leu Ser
806
807
                                           250
                        245
808
          Arg Val Val Leu Asp Gln Gln Leu Cys Phe Leu Gly Asn Ala Ala Leu
809
                                        265
          Asp Thr Thr Phe Asp Ile Asp Val Gln His Trp Glu Arg Val Gly Gly
810
```

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
275
                                         280
     811
                Gly Glu Glu Leu Phe Asn Val Lys Met Arg Glu Gly Ala Gln Gly Arg
     812
                                      295
                                                         300
     813
               Asp Ile Ala Val Ala Thr Val Lys Val Arg Phe Asp Ala Ala Ser Glu
     814
                                 310
                                                   315
     815
     816
                Gly Gly Arg Arg Gly
     817
                              325
     819 <210> SEQ ID NO: 10
     820 <211> LENGTH: 83
     821 <212> TYPE: Amino acid
     822 <213> ORGANISM: Myxococcus xanthus
€\ > 823 <400> SEQUENCE: 10
     824
               Met Thr Asp Glu Gln Ile Arg Gly Val Val His Gln Ser Ile Val Arg
     825
               Val Leu Pro Arg Val Arg Ser Asn Glu Ile Ala Gly His Leu Asn Leu
     826
     827
                                              25
                                                               30
               Arg Glu Leu Gly Ala Asp Ser Val Asp Arg Val Glu Ile Leu Thr Ser
     828
                                          40
     829
     830
                Ile Leu Asp Ser Leu Arg Leu Gln Lys Thr Pro Leu Ala Lys Phe Ala
     831
                                      55
                                                         60
               Asp Ile Arg Asn Ile Asp Ala Leu Val Ala Phe Leu Ala Gly Glu Val
     832
     833
                                 70
                                                    75
     834
               Ala Gly Gly
     836 <210> SEQ ID NO: 11
     837 <211> LENGTH;, 374
     838 <212> TYPE Amino acid
     839 <213> ORGANISM: Myxococcus xanthus
(F/4 > 840 <400 > SEQUENCE: 11
               Met Met Gln Glu Arg Gly Val Ala Leu Pro Phe Glu Asp Pro Val Thr
     841
     842
                                                  10
     843
               Asn Ala Val Asn Ala Ala Arg Pro Ile Leu Asp Ala Met Ser Pro Glu
     844
                                             25
     845
               Ala Arg Glu Arg Ile Glu Leu Leu Val Thr Ser Ser Glu Ser Gly Val
     846
                                         40
     847
               Asp Phe Ser Lys Ser Ile Ser Ser Tyr Ala His Glu His Leu Gly Leu
     848
               Ser Arg His Cys Arg Phe Leu Glu Val Lys Gln Ala Cys Tyr Ala Ala
     849
     850
                                  70
                                                      75
     851
               Thr Gly Ala Leu Gln Leu Ala Leu Gly Tyr Ile Ala Ser Gly Val Ser
     852
                                                  90
                               85
               Pro Gly Ala Lys Ala Leu Val Ile Ala Thr Asp Val Thr Leu Val Asp
     853
     854
                                           105
                                                              110
               Glu Ser Gly Leu Tyr Ser Glu Pro Ala Met Gly Thr Gly Gly Val Ala
     855
     856
                                         120
               Val Leu Leu Gly Asp Glu Pro Arg Val Met Lys Met Asp Leu Gly Ala
     857
     858
                                      135
                                                         140
     859
               Phe Gly Asn Tyr Ser Tyr Asp Val Phe Asp Thr Ala Arg Pro Ser Pro
     860
                                  150
                                                      155
     861
               Glu Ile Asp Ile Gly Asp Val Asp Arg Ser Leu Phe Thr Tyr Leu Asp
```

Input Set: N:\Crf4\10182002\1710262D.raw
Output Set: N:\CRF4\10212002\1710262D.raw

```
170
    862
                           165
               Cys Leu Lys His Ser Phe Ala Ala Tyr Gly Arg Arg Val Asp Gly Val
    863
                                            185
    864
               Asp Phe Val Ser Thr Phe Asp Tyr Leu Ala Met His Thr Pro Phe Ala
    865
                                         200
                                                            205
    866
               Gly Leu Val Lys Ala Gly His Arg Lys Met Met Arg Glu Leu Thr Pro
    867
    868
                                    215
                                                       220
               Cys Asp Val Asp Glu Ile Glu Ala Asp Phe Gly Arg Arg Val Lys Pro
    869
    870
                                 230
                                                   235
               Ser Leu Gln Tyr Pro Ser Leu Val Gly Asn Leu Cys Ser Gly Ser Val
    871
    872
                             245
                                               250
               Tyr Leu Ser Leu Cys Ser Ile Ile Asp Thr Ile Lys Pro Glu Arg Ser
    873
    874
                                          265
                                                             270
    875
               Ala Arg Val Gly Met Phe Ser Tyr Gly Ser Gly Cys Ser Ser Glu Phe
                      275
                                        280
                                                           285
    876
               Phe Ser Gly Val Ile Gly Pro Glu Ser Val Ser Ala Leu Ala Gly Leu
    877
    878
                                   295
    879
               Asp Ile Gly Gly His Leu Arg Gly Arg Arg Gln Leu Thr Phe Asp Gln
    880
                                                   315
                                310
    881
               Tyr Val Glu Leu Leu Lys Glu Asn Leu Arg Cys Leu Val Pro Thr Lys
    882
                              325
                                                 330
                                                                                  Same
               Asn Arg Asp Val Asp Val Glu Arg Tyr Leu Pro Leu Val Thr Arg Thr
    883
                                                               350
    884
                                            345
               Ala Ser Arg Pro Arg Met Leu Ala Leu Arg Arg Val Val Asp Tyr His
    885
                                        360
    886
                      355
    887
               Arg Gln Tyr Glu Trp Val
    888
                   370
    890 <210> SEQ ID NO: 12
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Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

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Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

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	973		Glu G	тu	Arg	val	ASn	Pro	Pne	HIS			PIO	Pne			GTA	rre
	974					4 ()5				410)			4	415		
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Same

305

962

963

Input Set : N:\Crf4\10182002\1710262D.raw
Output Set: N:\CRF4\10212002\1710262D.raw

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  1059
             Ile Val Val Ser Gly Pro Ala Gln Asp Ile Glu Arg Ala Arg Gln Cys
  1060
                                     200
  1061
             Phe Val Asp Arg Gly Ala Arg Tyr Val Pro Leu Asn Val Arg Ala Pro
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Same

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

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215
 1062
            Phe His Ser Arg Tyr Met Gln Pro Ala Ala Ser Glu Phe Glu Arg Phe
 1063
 1064
                               230
                                                 235
 1065
             Leu Ser Gln Phe Gln Tyr Ala Pro Leu Arg Cys Val Val Ile Ser Asn
 1066
                            245
                                               250
             Val Thr Gly Arg Pro Tyr Ala His Asp Asn Val Val Gln Gly Leu Ala
 1067
 1068
                                         265
             Leu Gln Leu Arg Ser Pro Val Gln Trp Thr Ala Thr Val Arg Tyr Leu
 1069
                                       280
                                                         285
 1070
             Leu Glu Gln Gly Val Glu Asp Phe Glu Glu Leu Gly Pro Gly Arg Val
 1071
                                  295
                                                     300
 1072
            Leu Thr Arg Leu Ile Thr Ala Asn Lys Arg Gly Ala Pro Ala Pro Ala
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                                                 315
 1074
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 1079 <211> LENGTH: 417
 1080 <212> TYPE: Amino acid
 1081 <213> ORGANISM: Myxococcus xanthus
> 1082 <400> SEQUENCE: 16
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             Thr Ser Ala Ile Gly Gln Gly Ala Ala Ser Phe Thr Ser Ala Leu Leu
 1086
                                         25
 1087
             Glu Gly Ala Ala Arg Phe Arg Val Met Glu Arg Pro Gly Arg Gln His
 1088
                                      40
 1089
             Gln Ala Asn Gly Gln Thr Thr Ala His Leu Gly Ala Glu Ile Ala Ser
 1090
                                   55
 1091
            Leu Ala Val Pro Glu Gly Val Thr Pro Gln Leu Trp Arg Ser Ala Thr
 1092
                               70
                                                 75
            Phe Ser Gly Gln Ala Ala Leu Val Thr Val His Glu Ala Trp Asn Ala
 1093
 1094
                                               90
 1095
            Ala Arg Leu Gln Ala Val Pro Gly His Arg Ile Gly Leu Val Val Gly
 1096
                                         105
                                                           110
            Gly Thr Asn Val Gln Gln Arg Asp Leu Val Leu Met Gln Asp Ala Tyr
 1097
 1098
                                      120
 1099
            Arg Glu Arg Val Pro Phe Leu Arg Ala Ala Tyr Gly Ser Thr Phe Met
 1100
                                  135
                                                    140
 1101
            Asp Thr Asp Leu Val Gly Leu Cys Thr Gln Gln Phe Ala Ile His Gly
 1102
                               150
                                                 155
            Met Ser Phe Thr Val Gly Gly Ala Ser Ala Ser Gly Leu Leu Ala Val
 1103
                                             170
 1104
                            165
                                                                175
            Ile Gln Ala Ala Glu Ala Val Leu Ser Arg Lys Val Asp Val Cys Ile
 1105
                                                           190
 1106
                                        185
            Ala Val Gly Ala Leu Met Asp Val Ser Tyr Trp Glu Cys Gln Gly Leu
 1107
                                                         205
 1108
                                      200
            Arg Ala Met Gly Ala Met Gly Thr Asp Arg Phe Ala Arg Glu Pro Glu
 1109
                                  215
 1110
                                                     220
            Arg Ala Cys Arg Pro Phe Asp Arg Glu Ser Asp Gly Phe Ile Phe Gly
 1111
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Input Set : N:\Crf4\10182002\1710262D.raw
Output Set: N:\CRF4\10212002\1710262D.raw

	•											_			_		
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1113	3	Glu	Ala	Cys	Gly	Ala	Val	Val			Ser	Ala	Glu		Ala	Arg	Arg
1114						45				250				25			
1115	5	Arg	Gly	Val	Thr	Pro	Arg	_		Leu	Ser	Gly	${\tt Trp}$	Ala	Met	Gln	Leu
1116	5				60				265				270				
1117	7	Asp	Ala	Ser	Arg	Gly	Pro	Leu	Ser	Ser	Ile	Glu	Arg	Glu	Ser	Gln	Val
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1119	9	Ile	Gly	Ala	Ala	Leu	Arg	His	Ala	Asp	Leu	Ala	Pro	Glu	Arg	Val	Asp
1120)		90.				295					00					
1123	L	\mathtt{Tyr}	Val	Asn	Pro			Ser	Gly	Ser	Arg	Gln	Gly	Asp	Ala	Ile	Glu
1122	2	305				310					315				320		
1123	3	Leu	Gly	Ala	Leu	Lys	Ala	Cys	Gly	Leu	Thr	His	Ala	Arg	Val	Asn	Thr
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1125		Thr	Lys			Thr	Gly			Leu	Ser	Ser			Ala	Val	Gly
1126					40				345				350				
1127	7	Leu			Thr	Leu	Val		Leu	Glu	Gln	_	_	Leu	His	Pro	Ser
1128				55				360					55				_
1129		Leu		Leu	Val	Asp			Asp	Ser	Ser		Arg	Trp	Val	Gly	Ala
1130			370					75				380	_		_		
1133			Ala	Glu	Ala			Leu	Gln	Asn		Leu	Val	Leu	Ala		Gly
1132		385				390		_	_	_	395				400		
1133		Phe	Gly	Gly			Thr	Ala			Val	Arg	Arg		Ala	Thr	Glu
1134					40	5			4	110				415	5		
1135		Ser															
	7 <210>																
	3 <211>																
	<212>							. 4 1									
/	<213>			_	-	occus	s xai	ntnus	3								
	L <400>					Com	Dro	Dro	ni a	7 22	N a n	Птт	Cln	Thr	Leu	λκα	Wa l
1142		met 1	GIII	Ата		<i>э</i> ег	PIO	PIO	піз	10	ASP	тут	GIII		L5	AIG	Val
1143 1144		_	Dho	C1.1			Thr	Cvc	Dho		Cln	LOU	uic	_	Pro	λen	λla
1145		AIG	Pile		20	GIII	T 111T	Cys	25		GIII	ьеи	птэ	30	FIO	дор	AIG
1146		λen	λen			Sar	Δra	Thr			Δen	Glu	Cvs		Gln	Va 1	Len
1147		кэр	ASII	35	116	Der	nig	40	пси	110	тэр		15	0111	0111	var	пси
1148		Thr	T.e.ii		Glu	Glu	His		Thr	Thr	Val		-	Glu	Gly	Leu	Pro
1149			50	O _I D	01.4	O_u	55				,	60		024	~- <i>1</i>		
1150		His		Phe	Cvs	Met			Asp	Phe	Ara		Ile	His	Asp	Arg	Val
1151		65	,	1	010		70				75				80		
1152			Asp	Glv	Arσ							Glu	Gln	Leu	Tyr		Leu
1153				1	-	35			1	90			-		95		
1154		Trp	Leu	Gln	Leu	Ala	Thr	Gly	Pro	Tyr	Val	Thr	Val	Ala	His	Val	Gln
1155					L00			4	105	-			11				
1156			_			3 1 -	C117	Glv		Glv	Phe	Val	Ser	Αla	Cve	A an	Ile
)	Gly	Lys	Ala	ASN	Ala	GIA	O T Y	шСи	$O_{\mathcal{X}}$					Cys	ASP	
1157		Gly	_	Ala L15	ASN	Ala	GIY) .	Ory			.25		Cys	АБР	
1157 1158	,	-	_ 1	L15			_	120				1	.25		Leu		
	, }	Val	_ 1	L15			_	120 Val			Ser	1	.25				
1158	, 3 3	Val	Leu .30	L15 Ala	Lys	Ala	Glu 135	120 Val	Gln	Phe	Ser	1 Leu .40	.25 Ser	Glu		Leu	Phe
1158 1159	, 3))	Val	Leu .30	L15 Ala	Lys	Ala Ala	Glu 135	120 Val	Gln	Phe	Ser	Leu .40 Leu	.25 Ser	Glu	Leu	Leu Ile	Phe

Input Set : N:\Crf4\10182002\1710262D.raw
Output Set: N:\CRF4\10212002\1710262D.raw

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Ile Gln Arq Ala His Tyr Leu Thr Leu Met Thr Arg Pro Ile Asp Ala
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     1163
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                Ala Gln Ala Leu Ser Trp Gly Leu Ala Asp Ala Val Asp Ala Asp Ser
     1164
                                            185
     1165
     1166
                Glu Lys Leu Leu Arg Leu His Leu Arg Arg Leu Arg Cys Leu Ser Lys
                                         200
     1167
                Pro Ala Val Thr Gln Tyr Lys Lys Tyr Ala Ser Glu Leu Gly Gly Gln
     1168
     1169
                                     215
                                                      220
                Leu Leu Ala Ala Met Pro Arg Ala Ile Ser Ala Asn Glu Ala Met Phe
     1170
     1171
                                  230
                                                  235
                Ser Asp Arg Ala Thr Leu Glu Ala Ile His Arg Tyr Val Glu Thr Gly
     1172
                                               250
     1173
                               245
     1174
                Arg Leu Pro Trp Glu Ser
     1175
                          260
     1177 <210> SEQ ID NO: 18
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     1179 <212> TYPE: Amino acid
     1180 <213> ORGANISM: Myxococcus xanthus
EG/-> 1181 <400> SEQUENCE: 18
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     1184
                His Glu Val Glu Glu Gly Val Ala Gln Ile Thr Leu Val Asp Arg Glu
     1185
                                            25
                Asn Lys Asn Met Phe Ser Glu Gln Leu Val Arg Glu Leu Ile Thr Val
     1186
     1187
                                                              45
     1188
                Phe Gly Lys Val Asn Gly Asn Glu Arg Tyr Arg Ala Val Leu Thr
     1189
                                       55
                                                          60
     1190
                Gly Tyr Asp Thr Tyr Phe Ala Leu Gly Gly Thr Lys Ala Gly Leu Leu
     1191
                                  70
                                                    75
                Ser Ile Cys Asp Gly Ile Gly Ser Phe Asn Val Thr Asn Phe Tyr Ser
     1192
     1193
                               85
                                                90
     1194
                Leu Ala Leu Glu Cys Asp Ile Pro Val Ile Ser Ala Met Gln Gly His
     1195
                                             105
    1196
                Gly Val Gly Gly Phe Ala Met Gly Leu Phe Ala Asp Phe Val Val
     1197
                                         120
                                                            125
                Leu Ser Arg Glu Ser Val Tyr Thr Thr Asn Phe Met Arg Tyr Gly Phe
     1198
     1199
                                     135
                                                        140
                Thr Pro Gly Met Gly Ala Thr Tyr Ile Val Pro Lys Arg Leu Gly Tyr
     1200
     1201
                                 150
                                                 155
     1202
                Ser Leu Gly His Glu Leu Leu Leu Asn Ala Arg Asn Tyr Arg Gly Ala
                                                 170
                                                                    175
     1203
                              165
                Asp Leu Glu Lys Arg Gly Val Pro Phe Pro Val Leu Pro Arg Lys Glu
     1204
     1205
                                             185
                Val Leu Pro His Ala Tyr Glu Ile Ala Arg Asp Leu Ala Ala Lys Pro
     1206
                                        200
                                                          205
     1207
     1208
                Arg Leu Ser Leu Val Thr Leu Lys Arg His Leu Val Arg Asp Ile Arg
                                     215
    1209
                                                         220
                Arg Glu Leu Pro Asp Val Ile Glu Arg Glu Leu Glu Met His Gly Ile
    1210
                                                   235
    1211
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Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

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		<210>				19												
		<211>																
		<212>																
OV		<213>			_		occus	s xai	nthus	3								
L /->		<400>																
	1220		Met	Leu	Asn	Leu	Ile	Asn	Asn	His	Ala	His	Gly	Tyr			Thr	Pro
	1221		1				5				10				. 15			
	1222		Val	Val	Leu	Ala	Cys	Asn	Asp	Ala		Leu	Phe	Glu		Leu	Arg	Gln
	1223					20				25					30			
	1224		Gly	Pro	Lys	Asp	Phe	Asp	_	Leu	Ala	Glu	Ala		Arg	Ala	Asn	Arg
	1225				35					40	•			45				
	1226		Gly	His	Leu	Arg	Val	Ala	Met	Arg	Met	Phe		Ser	Leu	Gly	Trp	Val
	1227			50				55	•				60					
	1228		-	Arg	Asp	Ala	_	_	Val	Tyr	Ala		Thr	Ala	Ala			Ala
	1229		65					70				75				80		
	1230		His	Arg	Ser			Arg	Glu	Ala		Ser	Leu	Phe	Ala		Pro	Met
	1231						35				90				_	95		
	1232		Asp	Arg	-		Arg	Gly	Glu	Asp	-	Leu	Ser			Pro	Trp	Phe
	1233					L00				105					L10	_		_
	1234		Glu	_		Arg	Ala	Ser	_	Asp	Thr	Asp	Asp		Leu	Val	Arg	Glu
	1235				1.15		_	_	120					125				
	1236				Asp	Gly	Ala		Ile	Thr	Pro			Leu	Ala	Leu	GLu	GIn
	1237			L30	_			135	_			_ 14				_	_	
	1238		_	Gly	Gly	Leu	_		Ala	Arg	Arg		Ser	Asp	Leu			GLY
	1239		145					50	_	-	_	155				16		_
	1240		Gly	Asp	Gly	_	_	Thr	Cys	Val			Ala	Val			GIu	Leu.
	1241					16				_	_170		_	0 3	17		1	
	1242		Ala	Gly			Ser	Ala	GIn	Lys		Thr	Arg			Ala	Val	Asp
	1243					L80	_	_		185			_,		190			-
	1244		Ala			Thr	Pro	Lys		Ala	Pne	тте			Arg	Ата	Leu	Leu
	1245		-1	-	L95	**- 1	a 1		200		D	16- ±		205	0	14- -	D	a 1
	1246		Phe		тте	vaı	GTA		Tyr	Arg	Pro			Ата	ser	мет	PIO	GIII
	1247		.	210	D1	01		215	.	a1	**- 1	22		3	3	61. .	7 J -	C1
	1248			Leu	Pne	GIY			ASP	Gln	vaı			Arg	ASP	GIU		GIY
	1249		225	a 1	τ	***		230	3	m b	T	23		т1.	C1	Com	240	ni a
	1250		HIS	GLU	Leu			Asp	Arg	Thr			vaı	тте			СТУ	птэ
	1251		01 =	TT 4 -	7	24		Dha	7 l a	C1	250		T	T ON	25		mh.~	Wa 1
	1252		GIII	HIS			TAL	Pne	Ата	Glu 265	Leu	GIU	гуѕ	ьец 27		TTE	1111	vaı
	1253		Dh.a	3 ~ ~		50	7	T	C		<i>c</i> 1 ~	Dwo	7 mar			7 l a	A an	Mot
	1254		Pne	Asp		GIU	ASN	Leu		Ala	GIII	Pro	_		тте	Ald	ASP	мес
	1255		a 1	G	275	•	01	m la sa		30	T	3		85	~1	mh	17-1	т
	1256		_	_	стλ	Asp	СΤΆ			Leu	гÀ2	arg		туг	GIU	THE	٧al	Leu
	1257			290	m k	3	7	29		7 1 -	T ~ · ·	3	300	Dh a	Dro	Τ	mb	Tou
	1258		_	HIS	Tnr	Arg			arg	Ala			arg	ьие	LLO			ьeu
	1259		305	31 -	3 T -	3	310		01	T		115	~1	7 l ~	λ 1 -	32		mh
	1260		тте	Ата	Ата			asn	GIU	Lys		ьeu	GIU	AIG			arg	THE
	1261					325					330				335	,		

RAW SEQUENCE LISTING

DATE: 10/21/2002 TIME: 16:29:22

PATENT APPLICATION: US/09/710,262D TIME:

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

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1264	Asp	Arg	Leu	Ile	Glu	Asp	Leu	Arg	Ala	Arg	Gly	Leu	Ala	Glu	Pro	Glu		
1265			355				360	0				365						
1266	Asn	Thr	Leu	His	Ile	Arg	Ser	Phe	Leu	Asp	His	Asp	Arg	Pro	Tyr	Gln		
1267		370			•	37	5		380								•	
1268	Pro	Pro	Ala	Asp	Arg	Ala	Gly	Leu	His	Ala	Arg	Ile	Pro	Phe	Asp	Ser	Same	/
1269	385		390						. ;	395				400)		17000	
1270	Val	Phe	Val	Gly	Lys	Ala	Gly	Gln	Glu	Val	Val	Pro	Ala	Glu	Val	Phe		
1271			405							410 415								
1272	His	Ser	Leu	Val	Glu	His	Leu	Glu										
1273				420														

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/710,262D

DATE: 10/21/2002 TIME: 16:29:23

Input Set : N:\Crf4\10182002\1710262D.raw
Output Set: N:\CRF4\10212002\1710262D.raw

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L:16 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:448 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:554 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:627 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:671 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:699 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:715 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:775 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:823 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:840 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:894 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:922 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:988 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1034 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1082 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1141 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1181 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1219 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
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